EM Connectomics Cheat Sheet

website: **microns-explorer.org**
Info Service URL: global.daf-apis.com/info

to get list of table_names: client.materialize.get_tables()	table_name	N	short description
	synapses_pni_2	337 M	automated synapse detections
	nucleus_detection_v0	144 K	nucleus detections
	nucleus_neuron_svm	172 K	predictions about what nuclei are neurons
	aibs_soma_nuc_metamodel_preds_v117	87 K	cell type predictions about nuclei/somas
	allen_v1_column_types_slanted	1,364	manual/expert cell type calls for neurons in “column”
	aibs_column_nonneuronal	545	manual/expert cell type calls for non-neurons in “column”
	proofreading_status_public_release	764	status of axon and dendrite proofreading on cells
	functional_coreg	9,518	primary functionally coregistered cells
	func_unit_em_match_release	200	extra functionally coregistered cells

see client.materialize.get_metadata(table_name)[’description’] for more

proofreading_status_public_release

Column	Description
valid	A bookkeeping column, should always be 't'
pt_position	This is the x,y,z location in voxels of the point that was annotated here as being at this cells soma location. Note, this table has a voxel resolution of 4,4,40 nm, and so you might want to convert this column to a nm position.
pt_supervoxel_id	You can generally ignore this column, we keep it for bookkeeping in order to make it easier to update this annotation when the segmentation changes.
pt_root_id	This is the unique ID of the 'root' object in the segmentation, sometimes we refer to this as a segmentation id or a cell id.
valid_id	This is the ID of the object when this proofreading status was applied, for this release, this column matches the pt_root_id and so can be ignored. Its here to help alert us if the object changed since the human who judged this neuron to be 'clean' for example. In such case its possible theoretically that the cell is no longer 'clean'.
status_dendrite	There are three possible status values for each compartment: 'non' indicates no comprehensive proofreading. 'clean' indicates that all false merges have been removed, but all tips have not necessarily been followed. 'extended' indicates that the cell is both clean and all tips have been followed as far as a proofreader was able to.
status_axon	Same as status_dendrite but for axon. You should only trust outputs of cells with at least clean, and cells with extended will have the largest number of trustable outputs for its cell type

synapses_pni_2

Column	Description
id	The ID that is specific to this synapse annotation
pre_pt_supervoxel_id	a bookkeeping column for the presynaptic side
pre_pt_root_id	the ID of the segment/root_id on the presynaptic side
post_pt_supervoxel_id	Same bookkeeping column as pre_pt but for the post synaptic side.
size	The size of the synaptic cleft in units of 4,4,40 voxels.
pre_pt_position	Same as pre_pt but for the post synaptic side.
ctr_pt_position	a point that is on the centroid of the synaptic cleft.

aibs_soma_nuc_metamodel_preds_v117

Column	Description
id	The ID that is specific to cell type call annotation
target_id	the target nucleus id that this annotation references
classification_system	one aibs_neuronal, or aibs_nonneuronal indicating its broad class
cell_type	a cell type call.. see cell type table below for legend
id_ref	the nucleus id that this annotation references (should match target_id)
valid__ref	bookkeeping..can ignore
pt_supervoxel_id	a bookkeeping column for the nucleus point
pt_root_id	the ID of the segmentation at the nucleus centroid 'pt_position'
pt_position	a point that is at the centroid of the nucleus segmentation (in 4,4,40 voxels by default)

cell_type	Description
aibs_neuronal	
23P	a layer 2/3 pyramidal neuron
4P	a layer 4 pyramidal neuron
5P-IT	layer 5 intertelencenphalic neuron (thin tufted)
5P-ET	a layer 5 extra-telecenphalic neuron (thick tufted, or pyramidal tract)
5P-NP	a layer 5 near projecting neuron
6P-IT	a layer 6 intertelencenphalic neuron
6P-CT	a layer 6 cortico-thalamic neuron
BC	a basket cell
MC	a martinotti cell
BPC	a bipolar cell
NGC	a neurogliaform cell
aibs_nonneuronal	
astrocyte	an astrocyte
oligo	an oligodendrocyte
pericyte	a pericyte adjacent to a blood vessel
microglia	a microglia
opc	a oligodendrocyte precursor cell

nglui.statebuilder.helpers

make_neuron_neuroglancer_link(client, root_id(s), view_kws={}, return_as=’html’ or ‘url’)
make_synapse_neuroglancer_link(synapse_df, client, view_kws={}, return_as=’html’ or ‘url’)

documentation links

caveclient docs:	caveclient.readthedocs.io
meshparty docs:	meshparty.readthedocs.io
nglui repo:	https://github.com/seung-lab/NeuroglancerAnnotationUI
neuroglancer:	https://www.microns-explorer.org/visualization
mm^3 dataset:	https://www.microns-explorer.org/cortical-mm3

view_kws valid keys

- *show_slices* : Boolean, sets if slices are shown in the 3d view. Defaults to False.
- *layout* : `xy-3d` / `xz-3d` / `yz-3d` (sections plus 3d pane), `xy` / `yz` / `xz` / `3d` (only one pane), or `4panel` (all panes). Default is `xy-3d` .
- *show_axis_lines* : Boolean, determines if the axis lines are shown in the middle of each view.
- *show_scale_bar* : Boolean, toggles showing the scale bar.
- *orthographic* : Boolean, toggles orthographic view (objects are the same size no matter distance from camera) in the 3d pane.
- *position* : 3-element vector, determines the centered location.
- *zoom_image* : Zoom level for the imagery in units of nm per voxel. Defaults to 8.
- *zoom_3d* : Zoom level for the 3d pane. Defaults to 2000. Smaller numbers are more zoomed in.